



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Falb, Dean
- (ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
DISEASE
- (iii) NUMBER OF SEQUENCES: 67
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/034,286
 - (B) FILING DATE: 04-MAR-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/870,434
 - (B) FILING DATE: 06-JUN-1997
 - (A) APPLICATION NUMBER: 08/799,910
 - (B) FILING DATE: 13-FEB-1997
 - (A) APPLICATION NUMBER: 60/011,787
 - (B) FILING DATE: 16-FEB-1996
 - (A) APPLICATION NUMBER: 08/599,654
 - (B) FILING DATE: 09-FEB-1996
 - (A) APPLICATION NUMBER: 08/485,573
 - (B) FILING DATE: 07-JUN-1995
 - (A) APPLICATION NUMBER: 08/386,844
 - (B) FILING DATE: 10-FEB-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: Other
 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 CATGCCTGTA GAAAAAGGTT 20

 (2) INFORMATION FOR SEQ ID NO:2:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: Other
 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 CTTCATAGAA TCTAAGCCTA 20

 (2) INFORMATION FOR SEQ ID NO:3:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: Other
 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 CCTGATAGAT GGGCACTGTG T 21

 (2) INFORMATION FOR SEQ ID NO:4:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: Other
 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 GAACACGGCA TTGTCACTAA CT 22

 (2) INFORMATION FOR SEQ ID NO:5:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: Other

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCATAGACT AGGCTCATAG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTAAAGAGA AATTCAAATC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGCCGTGTG GGTTAGTC

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTTATGGG AAGGTTTTTA CA

22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTTTCTGCG TCTCCCAT

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGACATCAGA AACTCCAACC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Glu Ala Arg Lys Leu Glu Glu Ala Lys Ser Arg Gly Ser Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Ser Ile His Pro Gln Ser Pro Ala Cys Arg Arg Asp Cys Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Val Lys Lys Asn Lys Glu Tyr Asn Val Gln Lys Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Ala His Arg His Arg Gly Leu Arg Pro Arg Arg Gln Lys Ala Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ile Pro Asp Ser Thr Glu Gln Ser Asp Val Arg Phe Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Pro Tyr Ala Glu Tyr Pro Lys Asn Pro Arg Ser Gln Glu Trp Gly
1 5 10 15
Arg Glu

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asn Pro Ser Phe Ile Ser Asp Glu Ser Arg Arg Arg Asp Tyr Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Phe Ser Asp Ala Ser Met Ser Pro Asp Ala Thr Lys Pro Ser His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Glu Gln Arg Ser Glu Ser Val Arg Arg Thr Arg Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Ser Gly Leu Gln His Ala Pro Glu Pro Asp Ala Ala Asp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGGCTGCGG CCGCTCCGAA GTCC

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCCGCCGGG GCCGCCACTA TCT

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCGGGACGCA GTGGGACAG

19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGGGGAGTTG ACGAAGATGG 20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTTTCATT CATACAA 17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATTTTCATT CATACAATAT ATG 23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATTTTCATT CATACAATAT ATGGCCTTT 29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATTTTCATT CATACAATAT ATGGCCTTTT GTGGC 35

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGACATTTC A TTTCATACAA TATATGGCCT TTTGT 35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTCATTTTCAT ACAATATATG GCCTTTTGT 29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCATACAATA TATGGCCTTT TGT 23

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AATATATGGC CTTTGT 17

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CATACGATAT CCTTTGGCGC CAGGGG

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGACCTGAAC ATACGATATC CTTTGGCGCC AGGGG

35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CATACGATAT CCTTTGGCGC CAGGGGTGGG GGGG

34

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CATGCGGGGC GAGGAGG

17

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CATGCGGGGC GAGGAGGCCA GGA

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
CATGCGGGGC GAGGAGGCCGA GGAGAAAAG 29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
CATGCGGGGC GAGGAGGCCGA GGAGAAAAGT CGTTT 35

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
GAACATGCGG GGCGAGGAGG CGAGGAGAAA AGTCG 35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
GCGGGGCGAG GAGGCGAGGA GAAAAGTCG 29

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
CGAGGAGGCG AGGAGAAAAG TCG 23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGCGAGGAGA AAAGTCG 17

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CAAAGCNGNN NNNNCNGAGN AGUC 24

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGUGGAGCCC CAGGGCAUUA CCUCAAGCN GNNNNNNCNG AGNAGUCGUG GGCAAGGUGG 60
GCACUCAGGU GGG 73

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GUGUCUCUAU GGGUUUGCCC AAAGCNGNNN NNNCNGAGNA GUCUCUGGAC AUUUCAUUUC 60
AUAC 64

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGCCCUCUCG CCGUCGGGCU CCUUGCUGAG CAAAGCNGNN NNNNCNGAGN AGUCGAUGCC 60
GAAGCCGAUC UUGCUGCGCG 80

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGACUUCGCC AAAGUCGCCG CAAAGCNGNN CNGAGNAGUC CAGCCCCGAG CGTTTGGACC 60
 TG 62

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGUUUGCCUG CUAAGGAGCG AACAAAGCNG NNNNNNCNGA GNAGUCGAUG UUUCUUUGUG 60
 AGUCGGGCGC CG 72

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCGGACGA GCGCAGAUCG UUUGGUCCUG AACAAAGCNG NNNNNNCNGA GNAGUCCGGG 60
 GCGAGGAGGC GAGGAGAAAA GUCG 84

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAGUAAGGA GGGGGGGGAG ACUCUAGUUC GCAAAGCNGN NNNNNCNGAG NAGUCAGUCG 60
 GCUAAGGUGA UGGGGGUUGC AGCACACC 88

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCTTAGATG	CAGCCTGCAA	ATTAAACTTT	GATTTTTTCAT	CTTGTGAAAG	CAGTCCTTGT	60
TCCTATGGCC	TAATGAACAA	CTTCCAGGTA	ATGAGTATGG	TGTCAGGATT	TACACCACTA	120
ATTTCTGCAG	GTATATTTTC	AGCCACTCTT	TCTTCAGCAT	TAGCATCCCT	AGTGAGTGCT	180
CCCAAAATAT	TTCAGGCTCT	ATGTAAGGAC	AACATCTACC	CAGCTTTCCA	GATGTTTGCT	240
AAAGGTTATG	GGAAAAATAA	TGAACCTCTT	CGTGGCTGCA	TCTAAGCC		288

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AAAAATAAAT	AAATTAAAGT	CTGAGACCAA	TTTGCCACTG	TGAATATAAG	CACATTAACC	60
CCAGGAGGAG	CCAAGAATA	CACAAACCTC	TCTATGAGAA	TTTACCAGTC	TTCTTTCATT	120
TGGCAAGAAA	AAGCTCAGGA	AAATTTGCTT	GTTTAAATTC	TATGAGCCTA	GTCTATGG	178

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGGTAATTCA	TTAATTACAC	TTTAAAATTG	GAAAGTGGGA	TAAGAAATCT	AAAGTAAACC	60
AGCTTATCTT	TGAAACAATA	TTATTTTGAA	ATTGGCTTTA	A		101

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGCTTGGTGG	TGATGCCTAC	AAGAAATGTT	TACATACAAA	CACTCTATAC	ATCTAACTCC	60
CGAAAAAGGA	CCAGCTATTT	CGGCAACAGA	AAAAAGACAA	GCATTTTCAGA	GGAGCGTTGC	120
TTTCCTTAAA	GACCTAACTC	ACTTAAGTCT	TACAAACAGA	AATAACAAGG	AGGACAATTT	180
TCTA						184

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Gly	Leu	Leu	Pro	Lys	Leu	Gly	Ala	Ser	Gln	Gly	Ser	Asp	Thr	Ser
1				5					10					15	
Thr	Ser	Arg	Ala	Gly	Arg	Cys	Ala	Arg	Ser	Val	Phe	Gly	Asn	Ile	Lys
		20						25					30		
Val	Phe	Val	Leu	Cys	Gln	Gly	Leu	Gln	Leu	Cys	Gln	Leu	Leu	Tyr	
		35					40				45				
Ser	Ala	Tyr	Phe	Lys	Ser	Ser	Leu	Thr	Thr	Ile	Glu	Lys	Arg	Phe	Gly
	50				55						60				
Leu	Ser	Ser	Ser	Ser	Ser	Gly	Leu	Ile	Ser	Ser	Leu	Asn	Glu	Ile	Ser
65					70					75				80	
Asn	Ala	Ile	Leu	Ile	Ile	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Arg	Val	His
			85					90						95	
Arg	Pro	Arg	Leu	Ile	Gly	Ile	Gly	Gly	Leu	Phe	Leu	Ala	Ala	Gly	Ala
			100					105					110		
Phe	Ile	Leu	Thr	Leu	Pro	His	Phe	Leu	Ser	Glu	Pro	Tyr	Gln	Tyr	Thr
		115					120					125			
Leu	Ala	Ser	Thr	Gly	Asn	Asn	Ser	Arg	Leu	Gln	Ala	Glu	Leu	Cys	Gln
	130				135						140				
Lys	His	Trp	Gln	Asp	Leu	Pro	Pro	Ser	Lys	Cys	His	Ser	Thr	Thr	Gln
145					150					155					160
Asn	Pro	Gln	Lys	Glu	Thr	Ser	Ser	Met	Trp	Gly	Leu	Met	Val	Val	Ala
			165					170						175	
Gln	Leu	Leu	Ala	Gly	Ile	Gly	Thr	Val	Pro	Ile	Gln	Pro	Phe	Gly	Ile
		180						185					190		
Ser	Tyr	Val	Asp	Asp	Phe	Ser	Glu	Pro	Ser	Asn	Ser	Pro	Leu	Tyr	Ile
		195					200					205			
Ser	Ile	Leu	Phe	Ala	Ile	Ser	Val	Phe	Gly	Pro	Ala	Phe	Gly	Tyr	Leu
	210				215						220				
Leu	Gly	Ser	Val	Met	Leu	Gln	Ile	Phe	Val	Asp	Tyr	Gly	Arg	Val	Asn
225					230					235					240
Thr	Ala	Ala	Val	Asn	Leu	Val	Pro	Gly	Asp	Pro	Arg	Trp	Ile	Gly	Ala
			245						250					255	
Trp	Trp	Leu	Gly	Leu	Leu	Ile	Ser	Ser	Ala	Leu	Leu	Val	Leu	Thr	Ser
		260						265					270		
Phe	Pro	Phe	Phe	Phe	Phe	Pro	Arg	Ala	Met	Pro	Ile	Gly	Ala	Lys	Arg
		275					280					285			
Ala	Pro	Ala	Thr	Ala	Asp	Glu	Ala	Arg	Lys	Leu	Glu	Glu	Ala	Lys	Ser
	290				295						300				
Arg	Gly	Ser	Leu	Val	Asp	Phe	Ile	Lys	Arg	Phe	Pro	Cys	Ile	Phe	Leu
305					310					315					320
Arg	Leu	Leu	Met	Asn	Ser	Leu	Phe	Val	Leu	Val	Val	Leu	Ala	Gln	Cys
				325					330					335	
Thr	Phe	Ser	Ser	Val	Ile	Ala	Gly	Leu	Ser	Thr	Phe	Leu	Asn	Lys	Phe
		340					345						350		
Leu	Glu	Lys	Gln	Tyr	Gly	Thr	Ser	Ala	Ala	Tyr	Ala	Asn	Phe	Leu	Ile
		355					360					365			
Gly	Ala	Val	Asn	Leu	Pro	Ala	Ala	Ala	Leu	Gly	Met	Leu	Phe	Gly	Gly
	370				375						380				
Ile	Leu	Met	Lys	Arg	Phe	Val	Phe	Ser	Leu	Gln	Ala	Ile	Pro	Arg	Ile
385					390					395					400
Ala	Thr	Thr	Ile	Ile	Thr	Ile	Ser	Met	Ile	Leu	Cys	Val	Pro	Leu	Phe
			405						410					415	
Phe	Met	Gly	Cys	Ser	Thr	Pro	Thr	Val	Ala	Glu	Val	Tyr	Pro	Pro	Ser
		420					425						430		
Thr	Ser	Ser	Ser	Ile	His	Pro	Gln	Ser	Pro	Ala	Cys	Arg	Arg	Asp	Cys
		435					440					445			
Ser	Cys	Pro	Asp	Ser	Ile	Phe	His	Pro	Val	Cys	Gly	Asp	Asn	Gly	Ile
	450				455						460				
Glu	Tyr	Leu	Ser	Pro	Cys	His	Ala	Gly	Cys	Ser	Asn	Ile	Asn	Met	Ser
465					470					475					480
Ser	Ala	Thr	Ser	Lys	Gln	Leu	Ile	Tyr	Leu	Asn	Cys	Ser	Cys	Val	Thr
			485						490					495	
Gly	Gly	Ser	Ala	Ser	Ala	Lys	Thr	Gly	Ser	Cys	Pro	Val	Pro	Cys	Ala

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCTTACCAT	CGATGCGGCC	GCGGATCCAG	GGCTCAGAGG	GAGGACGCAC	CCGCCAGCCA	60
GCCGGGAACC	TTCCCTCGCG	GGCTCCCAGG	GCGGGTCTCT	TCCTCTCTCT	AGCCCTGCTC	120
AGGCATTCCG	CAGGTCCAGC	AGAGGTACAC	CTCCTGCAGC	GGGTTCCAAG	TGCACCTCCA	180
GCCTGATGGA	CCTGACCAAG	GAGGCTTCCA	GGAGCACAGA	AGGGGCTGCA	ACCCAGGTAC	240
CCAGAGAGTG	AGCAGTCCA	CGCGGGACTG	TGCACGGTGG	CCGACACCCG	CAGGGACGCC	300
CACCGGACGA	GCACGCGGAG	GGCCCTCGCC	TCCACGGATG	CACCATGCCG	GTGTGAGGAG	360
CATCTGTTCT	TCCCACTCTC	TGCAGTTAAC	AAACCCAACC	CAAACCACCA	CAGGTGCTCC	420
TCCTGGGGAG	TTTCCTGTCT	GACAAATGCC	AGGCTCACTT	CAAGGAGAAT	CACGCTTCTT	480
TCTAAAGATG	GATTCACCAT	TTAAACAGA	GCTCTGGGAG	CCTTTCGGCA	AATCTTGAAA	540
GCTGCACGGC	GCAGAGACAT	GGATGTGACT	TCCCAAGCCC	GGGGCGTAGG	CCTGGAGATG	600
TACCCAGGCA	CCGCGCAGCC	TGCGGCCCCC	AACACCACCT	CCCCGAGCT	CAACCTGTCC	660
CACCCGCTCC	TGGGCACCGC	CCTGGCCAAT	GGGACAGGTG	AGCTCTCGGA	GCACCAGCAA	720
TACGTGATCG	GCCGTGTTCT	CTCGTGCCTC	TACACCATCT	TCCTCTTCCC	CATCGGCTTT	780
GTGGGCAACA	TCCTGATCCT	GGTGGTGAAC	ATCAGCTTCC	GCGAGAAGAT	GACCATCCCC	840
GACCTGTACT	TCATCAACCT	GGCGGTGGCG	GACCTCATCC	TGGTGGCCGA	CTCCCTCATT	900
GAGGTGTTCA	ACCTGCACGA	GCGGTACTAC	GACATCGCCG	TCCTGTGCAC	CTTCATGTCT	960
CTCTTCTCTG	GGGTCAACAT	GTACAGCAGC	GTCTTCTTCC	TCACCTGGAT	GAGCTTCGAC	1020
CGCTACATCG	CCCTGGCCAG	GGCCATGCGC	TGCAGCCTGT	TCCGCACCAA	GCACCACGCC	1080
CGGCTGAGCT	GTGGCCTCAT	CTGGATGGCA	TCCGTGTCTG	CCACGCTGGT	GCCCTTCACC	1140
GCCGTGCACC	TGCAGCACAC	CGACGAGGCC	TGCTTCTGTT	TCGCGGATGT	CCGGGAGGTG	1200
CAGTGGCTCG	AGGTCACGCT	GGGCTTCATC	GTGCCCTTCG	CCATCATCGG	CCTGTGCTAC	1260
TCCCTCATTG	TCCGGGTGCT	GGTCAGGGCG	CACCGGCACC	GTGGGCTGCG	GCCCCGGCGG	1320
CAGAAGGCGC	TCCGCATGAT	CCTCGCAGTG	GTGCTGGTCT	TCTTCGTCTG	CTGGCTGCCG	1380
GAGAACGTCT	TCATCAGCGT	GCACCTCCTG	CAGCGGACGC	AGCCTGGGGC	CGCTCCTTGC	1440
AAGCAGTCTT	TCCGCCATGC	CCACCCCCTC	ACGGGCCACA	TTGTCAACCT	CGCCGCCTTC	1500
TCCAACAGCT	GCCTAAACCC	CCTCATCTAC	AGCTTTCTCG	GGGAGACCTT	CAGGGACAAG	1560
CTGAGGCTGT	ACATTGAGCA	GAAAACAAAT	TTGCCGGCCC	TGGACCGCTT	CTGTACAGCT	1620
GCCCTGAAGG	CCGTCATTCC	AGACAGCACC	GAGCAGTCGG	ATGTGAGGTT	CAGCAGTGCC	1680
GTGTAGACAG	CCTTGCCCGC	ATAGGCCAGC	CCAGGGTGTG	ACTCGGGAGC	TGCACACACC	1740
TGGGTGGACA	CAAGGCACGG	CCACGTCATG	TCTCTAAACT	GCGGTCAGAT	GTGGCTTCTG	1800
GCTCCTCGGG	CCTCGCGAGG	GTCACGCTTG	CCTGGTCACC	CTGGGGCTGC	TTAGGAAACC	1860
TCAGGACTGG	TCACCTTGCA	CTCCTCACAC	AGAATTGCTA	CAATCCCAAA	GCGCTCGCCC	1920
CGCAGGGTCC	AAAGGCCAGC	GGTGACCAGC	CTGTACCCCA	GCTCCTCCCC	GCCAACCCTG	1980
CCTGCCGCTG	CACCTGCCCG	CTGCTGCAGG	AAACATTTCT	GACACCGTCG	ACCAGGAAAG	2040
CCACACGGAG	AGGCCACTGT	GGGTGAAGCG	CCTCAGTTAC	ACAGGAACCC	TAAAGCAAAT	2100
CTGCCACCGT	GGGGGAACTG	ACGCTGGAGA	TGCAAGGTGC	TGGTGGGTCT	GAGCTGGACG	2160
TCGCGGTGTG	TCCTCTGTGC	CCACGGTCTG	AGCTAGCTAG	CGCACCGCCG	AGTTAAAGAG	2220
GAGAAGGAAA	ACATGCTGCT	CTGGTGCACG	CCTGAGCGTC	CTCCATCTTC	CAGGATGGCA	2280
GCAATGGCGC	TGTGCGGCC	CACCAGGCC	ACGAGGAGCA	GCAGCGCTCG	GCCCCGAGCA	2340
GCAGGAAGGC	CCCTCTGTGG	AGCGCCCGCC	GTCTGCTCCG	GGGTGGTTCA	GTCAGTGCTT	2400
GTTGACATCA	ACATGGCAAT	TGCACTCATG	TGGACTGGGA	CCGTGCGAGC	TGCCGTGTGG	2460
GTTAGTCGGG	TGCCAGGACA	ATGAAATACT	CCAGCACCTG	TGGCTGACGA	ATTGCTTTCT	2520
ACAGAAGTAA	CAGCTGGGGA	CAACTGCGAT	GATGATGTAA	AAACCTTCCC	ATAAAATAAG	2580
CC						2582

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Asp	Val	Thr	Ser	Gln	Ala	Arg	Gly	Val	Gly	Leu	Glu	Met	Tyr	Pro
1				5					10					15	
Gly	Thr	Ala	Gln	Pro	Ala	Ala	Pro	Asn	Thr	Thr	Ser	Pro	Glu	Leu	Asn
		20						25				30			
Leu	Ser	His	Pro	Leu	Leu	Gly	Thr	Ala	Leu	Ala	Asn	Gly	Thr	Gly	Glu
	35					40						45			
Leu	Ser	Glu	His	Gln	Gln	Tyr	Val	Ile	Gly	Leu	Phe	Leu	Ser	Cys	Leu
	50					55					60				
Tyr	Thr	Ile	Phe	Leu	Phe	Pro	Ile	Gly	Phe	Val	Gly	Asn	Ile	Leu	Ile
65				70					75					80	
Leu	Val	Val	Asn	Ile	Ser	Phe	Arg	Glu	Lys	Met	Thr	Ile	Pro	Asp	Leu
			85					90						95	
Tyr	Phe	Ile	Asn	Leu	Ala	Val	Ala	Asp	Leu	Ile	Leu	Val	Ala	Asp	Ser
			100					105					110		
Leu	Ile	Glu	Val	Phe	Asn	Leu	His	Glu	Arg	Tyr	Tyr	Asp	Ile	Ala	Val
	115							120				125			
Leu	Cys	Thr	Phe	Met	Ser	Leu	Phe	Leu	Arg	Val	Asn	Met	Tyr	Ser	Ser
	130					135					140				
Val	Phe	Phe	Leu	Thr	Trp	Met	Ser	Phe	Asp	Arg	Tyr	Ile	Ala	Leu	Ala
145					150				155					160	
Arg	Ala	Met	Arg	Cys	Ser	Leu	Phe	Arg	Thr	Lys	His	His	Ala	Arg	Leu
			165						170					175	
Ser	Cys	Gly	Leu	Ile	Trp	Met	Ala	Ser	Val	Ser	Ala	Thr	Leu	Val	Pro
			180					185					190		
Phe	Thr	Ala	Val	His	Leu	Gln	His	Thr	Asp	Glu	Ala	Cys	Phe	Cys	Phe
	195						200					205			
Ala	Asp	Val	Arg	Glu	Val	Gln	Trp	Leu	Glu	Val	Thr	Leu	Gly	Phe	Ile
	210					215					220				
Val	Pro	Phe	Ala	Ile	Ile	Gly	Leu	Cys	Tyr	Ser	Leu	Ile	Val	Arg	Val
225					230					235				240	
Leu	Val	Arg	Ala	His	Arg	His	Arg	Gly	Leu	Arg	Pro	Arg	Arg	Gln	Lys
			245						250					255	
Ala	Leu	Arg	Met	Ile	Leu	Ala	Val	Val	Leu	Val	Phe	Phe	Val	Cys	Trp
			260					265					270		
Leu	Pro	Glu	Asn	Val	Phe	Ile	Ser	Val	His	Leu	Leu	Gln	Arg	Thr	Gln
	275						280					285			
Pro	Gly	Ala	Ala	Pro	Cys	Lys	Gln	Ser	Phe	Arg	His	Ala	His	Pro	Leu
	290					295					300				
Thr	Gly	His	Ile	Val	Asn	Leu	Ala	Ala	Phe	Ser	Asn	Ser	Cys	Leu	Asn
305					310					315				320	
Pro	Leu	Ile	Tyr	Ser	Phe	Leu	Gly	Glu	Thr	Phe	Arg	Asp	Lys	Leu	Arg
			325						330					335	
Leu	Tyr	Ile	Glu	Gln	Lys	Thr	Asn	Leu	Pro	Ala	Leu	Asp	Arg	Phe	Cys
		340					345					350			
His	Ala	Ala	Leu	Lys	Ala	Val	Ile	Pro	Asp	Ser	Thr	Glu	Gln	Ser	Asp
		355					360					365			
Val	Arg	Phe	Ser	Ser	Ala	Val									
	370					375									

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1481 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met	Ala	Ser	Pro	Arg	Ala	Ser	Arg	Trp	Pro	Pro	Pro	Leu	Leu	Leu	Leu
1				5					10					15	
Leu	Leu	Pro	Leu	Leu	Leu	Leu	Pro	Pro	Ala	Ala	Pro	Gly	Thr	Arg	Asp
		20					25					30			

Pro	Pro	Pro	Ser	Pro	Ala	Arg	Arg	Ala	Leu	Ser	Leu	Ala	Pro	Leu	Ala
		35					40					45			
Gly	Ala	Gly	Leu	Glu	Leu	Gln	Leu	Glu	Arg	Arg	Pro	Glu	Arg	Glu	Pro
	50					55					60				
Pro	Pro	Thr	Pro	Pro	Arg	Glu	Arg	Arg	Gly	Pro	Ala	Thr	Pro	Gly	Pro
65					70					75				80	
Ser	Tyr	Arg	Ala	Pro	Glu	Pro	Gly	Ala	Ala	Thr	Gln	Arg	Gly	Pro	Ser
				85					90					95	
Gly	Arg	Ala	Pro	Arg	Gly	Gly	Ser	Ala	Asp	Ala	Ala	Trp	Lys	His	Trp
			100					105					110		
Pro	Glu	Ser	Asn	Thr	Glu	Ala	His	Val	Glu	Asn	Ile	Thr	Phe	Tyr	Gln
		115					120						125		
Asn	Gln	Glu	Asp	Phe	Ser	Thr	Val	Ser	Ser	Lys	Glu	Gly	Val	Met	Val
	130					135					140				
Gln	Thr	Ser	Gly	Lys	Ser	His	Ala	Ala	Ser	Asp	Ala	Pro	Glu	Asn	Leu
145					150					155				160	
Thr	Leu	Leu	Ala	Glu	Thr	Ala	Asp	Ala	Arg	Gly	Arg	Ser	Gly	Ser	Ser
				165					170					175	
Ser	Arg	Thr	Asn	Phe	Thr	Ile	Leu	Pro	Val	Gly	Tyr	Ser	Leu	Glu	Ile
			180					185					190		
Ala	Thr	Ala	Leu	Thr	Ser	Gln	Ser	Gly	Asn	Leu	Ala	Ser	Glu	Ser	Leu
			195				200						205		
His	Leu	Pro	Ser	Ser	Ser	Ser	Glu	Phe	Asp	Glu	Arg	Ile	Ala	Ala	Phe
	210					215					220				
Gln	Thr	Lys	Ser	Gly	Thr	Ala	Ser	Glu	Met	Gly	Thr	Glu	Arg	Ala	Met
225					230					235				240	
Gly	Leu	Ser	Glu	Glu	Trp	Thr	Val	His	Ser	Gln	Glu	Ala	Thr	Thr	Ser
				245					250					255	
Ala	Trp	Ser	Pro	Ser	Phe	Leu	Pro	Ala	Leu	Glu	Met	Gly	Glu	Leu	Thr
			260					265					270		
Thr	Pro	Ser	Arg	Lys	Arg	Asn	Ser	Ser	Gly	Pro	Asp	Leu	Ser	Trp	Leu
			275			280							285		
His	Phe	Tyr	Arg	Thr	Ala	Ala	Ser	Ser	Pro	Leu	Leu	Asp	Leu	Ser	Ser
	290					295					300				
Pro	Ser	Glu	Ser	Thr	Glu	Lys	Leu	Asn	Asn	Ser	Thr	Gly	Leu	Gln	Ser
305					310					315				320	
Ser	Ser	Val	Ser	Gln	Thr	Lys	Thr	Met	His	Val	Ala	Thr	Val	Phe	Thr
				325					330					335	
Asp	Gly	Gly	Pro	Arg	Thr	Leu	Arg	Ser	Leu	Thr	Val	Ser	Leu	Gly	Pro
			340					345					350		
Val	Ser	Lys	Thr	Glu	Gly	Phe	Pro	Lys	Asp	Ser	Arg	Ile	Ala	Thr	Thr
		355					360						365		
Ser	Ser	Ser	Val	Leu	Leu	Ser	Pro	Ser	Ala	Val	Glu	Ser	Arg	Arg	Asn
					375						380				
Ser	Arg	Val	Thr	Gly	Asn	Pro	Gly	Asp	Glu	Glu	Phe	Ile	Glu	Pro	Ser
385					390					395				400	
Thr	Glu	Asn	Glu	Phe	Gly	Leu	Thr	Ser	Leu	Arg	Trp	Gln	Asn	Asp	Ser
				405					410					415	
Pro	Thr	Phe	Gly	Glu	His	Gln	Leu	Ala	Ser	Ser	Ser	Glu	Val	Gln	Asn
			420					425					430		
Gly	Ser	Pro	Met	Ser	Gln	Thr	Glu	Thr	Val	Ser	Arg	Ser	Val	Ala	Pro
		435					440						445		
Met	Arg	Gly	Gly	Glu	Ile	Thr	Ala	His	Trp	Leu	Leu	Thr	Asn	Ser	Thr
	450					455					460				
Thr	Ser	Ala	Asp	Val	Thr	Gly	Ser	Ser	Ala	Ser	Tyr	Pro	Glu	Gly	Val
465					470					475				480	
Asn	Ala	Ser	Val	Leu	Thr	Gln	Phe	Ser	Asp	Ser	Thr	Val	Gln	Ser	Gly
				485					490					495	
Gly	Ser	His	Thr	Ala	Leu	Gly	Asp	Arg	Ser	Tyr	Ser	Glu	Ser	Ser	Ser
			500					505					510		
Thr	Ser	Ser	Ser	Glu	Ser	Leu	Asn	Ser	Ser	Ala	Pro	Arg	Gly	Glu	Arg
			515				520					525			
Ser	Thr	Leu	Glu	Asp	Ser	Arg	Glu	Pro	Gly	Gln	Ala	Leu	Gly	Asp	Ser
	530					535					540				
Ser	Ala	Asn	Ala	Glu	Asp	Arg	Thr	Ser	Gly	Val	Pro	Ser	Leu	Gly	Thr
545					550					555				560	
His	Thr	Leu	Ala	Thr	Val	Thr	Gly	Asn	Gly	Glu	Arg	Thr	Leu	Arg	Ser

Val	Thr	Leu	Thr	565	Asn	Thr	Ser	Met	Ser	570	Thr	Thr	Ser	Gly	Glu	575	Ala	Gly
			580						585						590			
Ser	Pro	Ala	Ala	Ala	Met	Pro	Gln	Glu	Thr	Glu	Gly	Ala	Ser	Leu	His			
		595					600					605						
Val	Asn	Val	Thr	Asp	Asp	Met	Gly	Leu	Val	Ser	Arg	Ser	Leu	Ala	Ala			
	610					615					620							
Ser	Ser	Ala	Leu	Gly	Val	Ala	Gly	Ile	Ser	Tyr	Gly	Gln	Val	Arg	Gly			
	625				630					635					640			
Thr	Ala	Ile	Glu	Gln	Arg	Thr	Ser	Ser	Asp	His	Thr	Asp	His	Thr	Tyr			
				645					650					655				
Leu	Ser	Ser	Thr	Phe	Thr	Lys	Gly	Glu	Arg	Ala	Leu	Leu	Ser	Ile	Thr			
			660					665						670				
Asp	Asn	Ser	Ser	Ser	Ser	Asp	Ile	Val	Glu	Ser	Ser	Thr	Ser	Tyr	Ile			
		675					680					685						
Lys	Ile	Ser	Asn	Ser	Ser	His	Ser	Glu	Tyr	Ser	Ser	Phe	Ser	His	Ala			
	690					695					700							
Gln	Thr	Glu	Arg	Ser	Asn	Ile	Ser	Ser	Tyr	Asp	Gly	Glu	Tyr	Ala	Gln			
	705				710					715					720			
Pro	Ser	Thr	Glu	Ser	Pro	Val	Leu	His	Thr	Ser	Asn	Leu	Pro	Ser	Tyr			
				725					730					735				
Thr	Pro	Thr	Ile	Asn	Met	Pro	Asn	Thr	Ser	Val	Val	Leu	Asp	Thr	Asp			
			740					745					750					
Ala	Glu	Phe	Val	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser			
		755				760						765						
Ser	Ser	Ser	Ser	Gly	Pro	Pro	Leu	Pro	Leu	Pro	Ser	Val	Ser	Gln	Ser			
	770					775					780							
His	His	Leu	Phe	Ser	Ser	Ile	Leu	Pro	Ser	Thr	Arg	Ala	Ser	Val	His			
	785				790					795					800			
Leu	Leu	Lys	Ser	Thr	Ser	Asp	Ala	Ser	Thr	Pro	Trp	Ser	Ser	Ser	Pro			
				805					810					815				
Ser	Pro	Leu	Pro	Val	Ser	Leu	Thr	Thr	Ser	Thr	Ser	Ala	Pro	Leu	Ser			
			820					825					830					
Val	Ser	Gln	Thr	Thr	Leu	Pro	Gln	Ser	Ser	Ser	Thr	Pro	Val	Leu	Pro			
		835					840					845						
Arg	Ala	Arg	Glu	Thr	Pro	Val	Thr	Ser	Phe	Gln	Thr	Ser	Thr	Met	Thr			
	850					855					860							
Ser	Phe	Met	Thr	Met	Leu	His	Ser	Ser	Gln	Thr	Ala	Asp	Leu	Lys	Ser			
	865				870					875				880				
Gln	Ser	Thr	Pro	His	Gln	Glu	Lys	Val	Ile	Thr	Glu	Ser	Lys	Ser	Pro			
				885					890					895				
Ser	Leu	Val	Ser	Leu	Pro	Thr	Glu	Ser	Thr	Lys	Ala	Val	Thr	Thr	Asn			
		900						905					910					
Ser	Pro	Leu	Pro	Pro	Ser	Leu	Thr	Glu	Ser	Ser	Thr	Glu	Gln	Thr	Leu			
		915					920					925						
Pro	Ala	Thr	Ser	Thr	Asn	Leu	Ala	Gln	Met	Ser	Pro	Thr	Phe	Thr	Thr			
	930					935					940							
Thr	Ile	Leu	Lys	Thr	Ser	Gln	Pro	Leu	Met	Thr	Thr	Pro	Gly	Thr	Leu			
	945				950					955				960				
Ser	Ser	Thr	Ala	Ser	Leu	Val	Thr	Gly	Pro	Ile	Ala	Val	Gln	Thr	Thr			
				965					970					975				
Ala	Gly	Lys	Gln	Leu	Ser	Leu	Thr	His	Pro	Glu	Ile	Leu	Val	Pro	Gln			
			980					985					990					
Ile	Ser	Thr	Glu	Gly	Gly	Ile	Ser	Thr	Glu	Arg	Asn	Arg	Val	Ile	Val			
		995				1000						1005						
Asp	Ala	Thr	Thr	Gly	Leu	Ile	Pro	Leu	Thr	Ser	Val	Pro	Thr	Ser	Ala			
	1010					1015					1020							
Lys	Glu	Met	Thr	Thr	Lys	Leu	Gly	Val	Thr	Ala	Glu	Tyr	Ser	Pro	Ala			
				1030						1035					1040			
Ser	Arg	Ser	Leu	Gly	Thr	Ser	Pro	Ser	Pro	Gln	Thr	Thr	Val	Val	Ser			
				1045					1050					1055				
Thr	Ala	Glu	Asp	Leu	Ala	Pro	Lys	Ser	Ala	Thr	Phe	Ala	Val	Gln	Ser			
			1060					1065					1070					
Ser	Thr	Gln	Ser	Pro	Thr	Thr	Leu	Ser	Ser	Ser	Ala	Ser	Val	Asn	Ser			
		1075					1080					1085						
Cys	Ala	Val	Asn	Pro	Cys	Leu	His	Asn	Gly	Glu	Cys	Val	Ala	Asp	Asn			
	1090					1095					1100							

Thr Ser Arg Gly Tyr His Cys Arg Cys Pro Pro Ser Trp Gln Gly Asp
 105 1110 1115 1120
 Asp Cys Ser Val Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Pro Ser
 1125 1130 1135
 Thr Ala Thr Cys Asn Asn Thr Gln Gly Ser Phe Ile Cys Lys Cys Pro
 1140 1145 1150
 Val Gly Tyr Gln Leu Glu Lys Gly Ile Cys Asn Leu Val Arg Thr Phe
 1155 1160 1165
 Val Thr Glu Phe Lys Leu Lys Arg Thr Phe Leu Asn Thr Thr Val Glu
 1170 1175 1180
 Lys His Ser Asp Leu Gln Glu Val Glu Asn Glu Ile Thr Lys Thr Leu
 185 1190 1195 1200
 Asn Met Cys Phe Ser Ala Leu Pro Ser Tyr Ile Arg Ser Thr Val His
 1205 1210 1215
 Ala Ser Arg Glu Ser Asn Ala Val Val Ile Ser Leu Gln Thr Thr Phe
 1220 1225 1230
 Ser Leu Ala Ser Asn Val Thr Leu Phe Asp Leu Ala Asp Arg Met Gln
 1235 1240 1245
 Lys Cys Val Asn Ser Cys Lys Ser Ser Ala Glu Val Cys Gln Leu Leu
 1250 1255 1260
 Gly Ser Gln Arg Arg Ile Phe Arg Ala Gly Ser Leu Cys Lys Arg Lys
 265 1270 1275 1280
 Ser Pro Glu Cys Asp Lys Asp Thr Ser Ile Cys Thr Asp Leu Asp Gly
 1285 1290 1295
 Val Ala Leu Cys Gln Cys Lys Ser Gly Tyr Phe Gln Phe Asn Lys Met
 1300 1305 1310
 Asp His Ser Cys Arg Ala Cys Glu Asp Gly Tyr Arg Leu Glu Asn Glu
 1315 1320 1325
 Thr Cys Met Ser Cys Pro Phe Gly Leu Gly Gly Leu Asn Cys Gly Asn
 1330 1335 1340
 Pro Tyr Gln Leu Ile Thr Val Val Ile Ala Ala Gly Gly Gly Leu
 345 1350 1355 1360
 Leu Leu Ile Leu Gly Ile Ala Leu Ile Val Thr Cys Cys Arg Lys Asn
 1365 1370 1375
 Lys Asn Asp Ile Ser Lys Leu Ile Phe Lys Ser Gly Asp Phe Gln Met
 1380 1385 1390
 Ser Pro Tyr Ala Glu Tyr Pro Lys Asn Pro Arg Ser Gln Glu Trp Gly
 1395 1400 1405
 Arg Glu Ala Ile Glu Met His Glu Asn Gly Ser Thr Lys Asn Leu Leu
 1410 1415 1420
 Gln Met Thr Asp Val Tyr Tyr Ser Pro Thr Ser Val Arg Asn Pro Glu
 425 1430 1435 1440
 Leu Glu Arg Asn Gly Leu Tyr Pro Ala Tyr Thr Gly Leu Pro Gly Ser
 1445 1450 1455
 Arg His Ser Cys Ile Phe Pro Gly Gln Tyr Asn Pro Ser Phe Ile Ser
 1460 1465 1470
 Asp Glu Ser Arg Arg Arg Asp Tyr Phe
 1475 1480

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGCCCCGCG	CCGTCACCAT	GGCCTCGCCG	CGCGCCTCGC	GGTGGCCGCC	GCCGCTCCTG	60
CTGCTGTTGC	TGCCGCTGCT	GCTGCTGCCG	CCGGCGGGCC	CCGGGACGCG	GGACCCGCCG	120
CCTTCCCCGG	CTCGCCGCGC	GCTGAGCCTG	GCGCCCCCTG	CGGGAGCGGG	GCTGGAGCTG	180
CAGCTGGAGC	GCCGCCCGGA	GCGCGAGCCG	CCGCCCCACG	CGCCCCGGGA	GCGCCGCGGG	240
CCCGCGACCC	CCGGCCCCAG	CTACAGGGCC	CCTGAGCCAG	GCGCCGCGAC	ACAGCGGGGA	300
CCCTCCGGCC	GGGCCCCCAG	AGGCGGGGAG	GCGGATGCTG	CCTGGAACA	TTGGCCAGAA	360

AGTAACACTG	AGGCCCATGT	AGAAAACATC	ACCTTCTATC	AGAATCAAGA	GGACTTTTCA	420
ACAGTGTCCT	CCAAAGAGGG	TGTGATGGTT	CAGACCTCTG	GGAAAGAGCCA	TGCTGCTTCG	480
GATGCTCCAG	AAAACCTCAC	TCTACTCGCT	GAACACAGCAG	ATGCTAGAGG	AAGGAGCGGC	540
TCTTCAAGTA	GAACAAACTT	CACCATTTTG	CCTGTTGGGT	ACTCACTGGA	GATAGCAACA	600
GCTCTGACTT	CCCAGAGTGG	CAACTTAGCC	TCGAAAGTGC	TTCACCTGCC	ATCCAGCAGT	660
TCAGAGTTCTG	ATGAAAGAAT	TGCCGCTTTT	CAAACAAAGA	GTGGAACAGC	CTCGGAGATG	720
GGAAACAGAGA	GGGCGATGGG	GCTGTCAGAA	GAATGGACTG	TGCACAGCCA	AGAGGCCACC	780
ACTTCGGCTT	GGAGCCCGTC	CTTTCTTCCT	GCTTGGGAGA	TGGGAGAGCT	GACCACGCCT	840
TCTAGGAAGA	GAAATTCCTC	AGGACCAGAT	CTCTCCTGGC	TGCATTTCTA	CAGGACAGCA	900
GCTTCCTCTC	CTCTCTTAGA	CCTTTCCTCA	CCTTCTGAAA	GTACAGAGAA	GCTTAACAAC	960
TCCACTGGCC	TCCAGAGCTC	CTCAGTCAGT	CAAACAAAGA	CAATGCATGT	TGCTACCGTG	1020
TTCACTGATG	GTGGCCCGAG	AACGCTGCGA	TCTTTGACGG	TCAGTCTGGG	ACCTGTGAGC	1080
AAGACAGAAG	GCTTCCCAAG	GGACTCCAGA	ATTGCCACGA	CTTCATCCTC	AGTCTCTCTT	1140
TCACCTCTCTG	CAGTGGAATC	GAGAAGAAAC	AGTAGAGTAA	CTGGGAATCC	AGGGGATGAG	1200
GAATTCATTG	AACCATCCAC	AGAAAATGAA	TTTGGACTTA	CGTCTTTGCG	TTGGCAAAAT	1260
GATTCCCCAA	CCTTTGGAGA	ACATCAGCTT	GCCAGCAGCT	CTGAGGTGCA	AAATGGAAGT	1320
CCCATGTCTC	AGACTGAGAC	TGTGTCTAGG	TCAGTCCGAC	CCATGAGAGG	TGGAGAGATC	1380
ACTGCACACT	GGCTCTTGAC	CAACAGCACA	ACATCTGCAG	ATGTGACAGG	AAGCTCTGCT	1440
TCATATCCTG	AAGGTGTGAA	TGCTTCAGTG	TTGACCCAGT	TCTCAGACTC	TACTGTACAG	1500
TCTGGAGGAA	GTCACACAGC	ATTGGGAGAT	AGGAGTTATT	CAGAGTCTTC	ATCTACATCT	1560
TCCTCGGAAA	GCTTGAATTC	ATCAGCACCA	CGTGGAGAAC	GTTCAACCTT	GGAAGACAGC	1620
CGAGAGCCAG	GCCAAGCACT	AGGTGACAGT	TCCGCCAATG	CAGAGGACAG	GACTTCTGGG	1680
GTGCCCTCTC	TCGGCACCCA	CACCTTGGCT	ACTGTCACTG	GAAACGGGGA	ACGCACACTG	1740
CGGTCTGTCA	CCCTCACCAA	CACCAGCATG	AGCACGACTT	CTGGGGAAGC	AGGCAGCCCT	1800
GCAGCGGCCA	TGCCCAAGA	AACAGAGGGT	GCCTCTCTGC	ACGTAAACGT	GACGGACGAC	1860
ATGGGCCTGG	TCTCACGGTC	ACTGGCCGCG	TCCAGTGCAC	TCGGAGTCGC	TGGGATTAGC	1920
TACGGTCAAG	TGCTGGGAC	AGCTATTGAA	CAAAGGACTT	CCAGCGACCA	CACAGACCAC	1980
ACCTACCTGT	CATCTACTTT	CACCAAAGGA	GAACGGGCGT	TACTGTCCAT	TACAGATAAC	2040
AGTTCATCCT	CAGACATTGT	GGAGAGCTCA	ACTTCTTATA	TTAAAATCTC	AAACTCTTCA	2100
CATTCAAGAT	ATTCTCTCCT	TTCTCATGCT	CAGACTGAGA	GAAGTAACAT	CTCATCCTAT	2160
GACGGGGAAT	ATGCTCAGCC	TTCTACTGAG	TCGCCAGTTC	TGCATACATC	CAACCTTCCG	2220
TCTTACACAC	CCACCATTAA	TATGCCGAAC	TATCTCGTTG	TTCTGGACAC	TGATCTGAGT	2280
TTTGTTAGTG	ACTCTCTCCT	CTCCTCTTCC	TCCTCCTCCT	CTTCTTCTTC	TTCAGGGCCT	2340
CCTTTGCCTC	TGCCCTCTGT	GTCACAATCC	CACCATTTAT	TTTCATCAAT	TTTACCATCA	2400
ACCAGGGCCT	CTGTGCATCT	ACTAAAGTCT	ACCTCTGATG	CATCCACACC	ATGGTCTTCC	2460
TCACCATCAC	CTTTACCAGT	ATCCTTAAAG	ACATCTACAT	CTGCCCCACT	TTCTGTCTCA	2520
CAAACAACCT	TGCCACAGTC	ATCTTCTACC	CCTGTCTGCG	CCAGGGCAAG	GGAGACTCCT	2580
GTGACTTCAT	TTCAGACATC	AACAATGACA	TCATTTCATGA	CAATGCTCCA	TAGTAGTCAA	2640
ACTGCAGACC	TTAAGAGCCA	GAGCACCCCA	CACCAAGAGA	AAGTCATTAC	AGAATCAAAG	2700
TCACCAAGCC	TGGTGTCTCT	GCCCCACAGG	TCCACCAAAG	CTGTAACAAC	AAACTCTCCT	2760
TTGCCTCCAT	CCTTAACAGA	GTCCTCCACA	GAGCAAACCC	TTCCAGCCAC	AAGCACCAC	2820
TTAGCACAAA	TTTCTCCAAC	TTTCACTAAT	ACCATTCTGA	AGACCTCTCA	GCCTCTTATG	2880
ACCACTCCTG	GCACCCCTGTC	AAGCACAGCA	TCTCTGGTCA	CTGGCCCTAT	AGCCGTACAG	2940
ACTACAGCTG	GAAAACAGCT	CTCGCTGACC	CATCCTGAAA	TACTAGTTCC	TCAAATCTCA	3000
ACAGAAGGTG	GCATCAGCAC	AGAAAGGAAC	CGAGTGATTG	TGGATGCTAC	CACCTGGATTG	3060
ATCCCTTTGA	CCAGTGTACC	CACATCAGCA	AAAGAAATGA	CCACAAAGCT	TGGCGTTACA	3120
GCAGAGTACA	GCCCAGCTTC	ACGTTCCCTC	GGAACATCTC	CTTCTCCCCA	AACCACAGTT	3180
GTTTCCACGG	CTGAAGACTT	GGCTCCCAAA	TCTGCCACCT	TTGCTGTTCA	GAGCAGCACA	3240
CAGTCACCAA	CAACACTGTC	CTCTTCAGCC	TCAGTCAACA	GCTGTGCTGT	GAACCCTTGT	3300
CTTCACAATG	GCGAATGCGT	CGCAGACAAC	ACCAGCCGTG	GCTACCACTG	CAGGTGCCCG	3360
CCTTCCTGGC	AAGGGGATGA	TTGCAGTGTG	GATGTGAATG	AGTGCCTGTC	GAACCCCTGC	3420
CCATCCACAG	CCACGTGCAA	CAATACTCAG	GGATCCTTTA	TCTGCAAATG	CCCGGTTGGG	3480
TACCAGTTGG	AAAAAGGGAT	ATGCAATTTG	GTTAGAACCT	TCGTGACAGA	GTTTAAATTA	3540
AAGAGAACTT	TTCTTAATAC	AACTGTGGAA	AAACATTTCAG	ACCTACAAGA	AGTTGAAAAT	3600
GAGATCACCA	AAACGTTAAA	TATGTGTTTT	TCAGCGTTAC	CTAGTTACAT	CCGATCTACA	3660
GTTTACGCCT	CTAGGGAGTC	CAACGCGGTG	GTGATCTCAC	TGCAAACAAC	CTTTTCCCTG	3720
GCCTCCAATG	TGACGCTATT	TGACCTGGCT	GATAGGATGC	AGAAATGTGT	CAACTCCTGC	3780
AAGTCCTCTG	CTGAGGTCTG	CCAGCTCTTG	GGATCTCAGA	GGCGGATCTT	TAGAGCGGGC	3840
AGCTTGTGCA	AGCGGAAGAG	TCCCGAATGT	GACAAAGACA	CCTCCATCTG	CAGTACCTG	3900
GACGGCGTTG	CCCTGTGCCA	GTGCAAGTCG	GGATCACTTC	AGTTCAACAA	GATGGACCAC	3960
TCCTGCCGAG	CATGTGAAGA	TGGATATAGG	CTTGAAAATG	AAACCTGCAT	GAGTTGCCCA	4020
TTTGGCCTTG	GTGGTCTCAA	CTGTGGAAC	CCCTATCAGC	TTATCACTGT	GGTGATCGCA	4080
GCCGCGGGAG	GTGGGCTCCT	GCTCATCCTA	GGCATCGCAC	TGATTGTTAC	CTGTTGCAGA	4140
AAGAATAAAA	ATGACATAAG	CAAACCTCAT	TTCAAAAGTG	GAGATTTCCA	AATGTCCCCA	4200
TATGCTGAAT	ACCCCAAAAA	TCCTCGCTCA	CAAGAATGGG	GCCGAGAAGC	TATTGAAATG	4260
CATGAGAATG	GAAGTACCAA	AAACCTCCTC	CAGATGACGG	ATGTGTACTA	CTCGCCTACA	4320
AGTGTAAGGA	ATCCAGAACT	TGAACGAAAC	GGACTCTACC	CGGCCTACAC	TGGACTGCCA	4380

GGATCACGGC	ATTCTTGCAT	TTTCCCCGGA	CAGTATAACC	CGTCTTTCAT	CAGTGATGAA	4440
AGCAGAAGAA	GAGACTACTT	TTAAGTCCAG	GAGAGAGAGG	GACTCATTGC	TCTGAGCCAG	4500
TCACCTGGGA	CCTCTGCTCA	GAGGACCGCA	CCAGGAGGCT	GCGCCCAGGA	TTTGTGCGGA	4560
GCCACGCTGA	GTGGCAAGCA	GGAAGAGGGA	CAGGCATGCG	GGGCGTGACC	ACAGTGGAGG	4620
AGACAGGTGG	ATGTGGAACC	ACAGGCTGCT	CATTACAGCAC	CTTTGTTGTT	ACTGTGAACG	4680
TGAATGTGGG	CCAGTATCAA	GAGAGTCTCT	CTGAGTGAAT	GCACCATGGC	ACTGGCACCA	4740
GGGCGACTAT	TAGCCAGGGC	AGACCACTAG	ACTTCAGTGC	AGGGACCTGG	TTTTCCCTTC	4800
GTTTGCACTT	TAGTAAATTG	GGTGGGAGGT	TTCTTTTGG	ATCTGTTTTG	AGACTGTTCC	4860
AGAAAGAAGG	CTTCCTTTCC	CGAGACACTT	CCATAGGCAG	CAATTTGGTG	ATTCAATTGC	4920
ASCAAAATAC	TGGCTTGTTA	ATTATTTTCC	TGCCCAGCRC	CTGCGTGCTA	AACAACAGAT	4980
GAGGATGASC	GTACCACTGA	AGTCTGAAGA	TGTCGCCATT	GAACGGACAG	TGTTTTTCATA	5040
TGTTTCTAGG	TTGTCTTATG	CTACAGTTTC	CAAGCCASCC	CCCACAGTGA	GGAAATGTGT	5100
GAGGACCCGC	ACACAACATG	AATGTGTTTT	TTAAGTCAAG	GTGACACATG	TATTTAAGAT	5160
TTTTTTTTTA	AATCTCYTTG	CAGTTAAATT	TCACCTTTC	AAACAAGCCT	GGATCAGGGC	5220
AAAACAACCT	ATATYTGTTT	TTAGCTGGAG	GCTCAGCAGG	CAGATTGCAG	GCAGGGGGGC	5280
ACTTTTCATC	CATGAGGGCC	CAGCCTGGGG	CCTGGGACTC	TGATCACCAT	TGTGGAGGCC	5340
AGAGGCAMCT	GCGTATGGAG	GAGAAATGTC	AAACTGAACG	CAGGTTTCAC	CACTCTAGGA	5400
AAGCAGCTTG	TTGACCCCTG	GCASCTGGAT	GTGGTTAGAG	GGATGGGCTG	AATAGSCAGG	5460
TTAGATTTCC	TGCATCAACA	GTGCTTTGGG	AASCTGTGTG	GATTCCCTGAG	GAAGAACAGG	5520
GAGCCGAGAT	GGAGCCACAC	ATGAATTYGC	TCACCGGCTA	CTGCAGCACT	TTGTACCCAG	5580
AATCTCATGT	CCACAAACCC	CATGTAAACT	TTCAACCACT	CAAAGSTGTT	TATTCGGCTG	5640
AAGAAATAAC	TTTTKTTTCT	CACCCAGTCA	TTTGTACCTC	TTCATATGGS	TATGTGCGAC	5700
CCTCCAGAAA	CGTGTTTATA	CTKCCAGTCA	GTGTGGGAGA	ACTGAAGACT	TCCGGTTGGT	5760
CGAGGAACTG	AGGGTTGACC	TTGCGGAAGG	AAGTTCCACT	CATCTTATTT	ATTATGCCTG	5820
TGATGTGGGT	CCTGCCAGGG	AGACATCCAG	TACTCGGTGT	CTKTAATTGC	CACCTGGGGA	5880
ACTGTGTTTA	TTGGCCTTCT	TTGGGGCATC	CTGGKTTCCG	ATGAAGTGAG	GGGAATACAG	5940
AGGTAAAAGA	ATTGTCTCCA	CCCTGAAGCG	GGGAGTCCCG	CTTCACATTT	CTGGAATGG	6000
TGCAGCCACT	GGGGACAGTT	CTGCCCCGGG	CATGGTTGTT	TCTTCAAGGT	CCTCTAAATA	6060
TAATCCCTAT	TCTTACATAA	TCCTTGGCCC	TGATGGTTTT	AAGCAAGAAC	TCCTGTGTCC	6120
MATGGTCTCC	ACCACTCACC	ATCACCCCTG	TGTAGCAAGA	GTCCTAGTCA	GGGGAGGTGC	6180
ATTTTAGTAG	TTACATTGCA	CTTATCCATG	AGATAAATAA	AAGGAGAVCT	GTTTTTATCA	6240
GTGGAGGCTA	ACCTAAAATT	TCAAAGTGTC	GCCTTTTGA	AATCTTGGGC	CTCTCTCTCT	6300
GTAGAACCAG	TGCCCTTTTG	TGGCTCACGG	CCTCGCACCT	AACTGGAGAG	TTCTGAGCTC	6360
CTGCAGCTCA	CCTGAGCCCA	CAGACTAGGC	TTCTTGGCTC	CTTCCGC		6407

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAATTCGGCA	CGAGGMCAGG	AGCTCCTTTW	CTGCGTCTCC	CATCATGGGG	CTTAGGGTTG	60
AGTCTTCAGG	TTCTGGGGGC	AGGAAGGACG	GGCACTCAGG	AGGCCCCCTC	CCCATCCACA	120
GCCCCCTCTT	GGGAGGGGGG	AAACTTGCCA	ACCCGGGAGG	CATGTGGATC	TTTTCTTAAG	180
CAAGATGCTG	AGCTGGAAAG	ATGGGGGTGT	AAGGTAATGT	CCCAAACCTG	AACTTTGCCA	240
GGCACTGGGA	GAGGCTGTGA	ACTCTTTTCT	GGCTTTAGAA	TTTAGGTCTA	GATCCCAAAA	300
GGCTAAGTAC	CCCCCTGGGG	CTAACCAAGG	GCATGCCTGG	GCTGAGCTGA	ACCTTCTGGT	360
GCACCTGGCC	CTGGCTGACT	GCTCTTCTGC	AGGAAGTTGG	AGGAGATTCC	TGAAGTTGAT	420
TCCTCAGGCT	GGATGTCCAA	GGGGGTTGGA	GTTTCTGATG	TCTTTCTGTC	TCCCTCTCTT	480
TTCTTTCTCT	CCCTACCAGG	TCCACTTCTT	TCAGAGGGGC	CTGCGGTGCT	CTAAAAGTTC	540
TCCTGTAAAA	GTTTAGAGCA	AATTGGTTAT	TATTTTAAAA	TCAATAAAAC	TTTTTAAAGT	600
ACTAAGACAA	CTTCTAAGAG	GGGAGTGGAC	AGAGGGCCTG	GTGGCAGCTC	ACAGTTTCTT	660
TTCTGACCTT	TGGTCTCACC	CACCAAGTGT	CCCACCTGAG	TGCCCACCTT	GCCCACCTGA	720
GGTAATGCCC	TGGGCTCTCCA	CCAGTCCAGT	TCCACAGGGC	GCAACCATGT	GGGAGTGGCG	780
GCTGATTGTT	ACCCAGTAGT	GTTGATAGCA	CATTATTTCAT	AACAGCCAAA	GAGAGGAAGC	840
AACCCAAATG	TCCATTAGCT	GATAAATGGA	TAAATGAAAT	ATGGTACGTC	CGAAGAATGG	900
AATATCATTC	ACCCATGAAA	AAGAACGAAG	TCCAGCACCA	AAACGTGCTA	CAACATGGAT	960
GAATCTCGAT	GACTTTGTGC	CACATGAAAG	AAGAAGCCAG	CCACAAAAGG	CCATATATTG	1020
TATGAAATGA	AATGTCCAGA	ATGGGCAAAC	CCATAGAGAC	ACAAAAATCT	CCGCCACCTC	1080
CCTACTCTCG	GCTGTCTCCT	CGCGACGAGT	ACAAGCCACT	GGATCTGTCC	GATTCCACAT	1140

TGTCTTACAC	TGAAACGGAG	GCTACCAACT	CCCTCATCAC	TGCTCCGGGT	GAATTCTCAG	1200
ACGCCAGCAT	GTCTCCGGAC	GCCACCAAGC	CGAGCCACTG	GTGCAGCGTG	GCGTACTGGG	1260
AGCACCGGAC	GCGCGTGGGC	CGCCTCTATG	CGGTGTACGA	CCAGGCCGTC	AGCATCTTCT	1320
ACGACCTACC	TCAGGGCAGC	GGCTTCTGCC	TGGGCCAGCT	CAACCTGGAG	CAGCGCAGCG	1380
AGTCGGTGCG	GCGAACGCGC	AGCAAGATCG	GCTTCGGCAT	CCTGCTCAGC	AAGGAGCCCG	1440
ACGGCGTGTG	GGCCTACAAC	CGCGGCGAGC	ACCCCATCTT	CGTCAACTCC	CCGACGCTGG	1500
ACGCGCCCGG	CGGCCGCGCC	CTGGTCTGTC	GCAAGGTGCC	CCCCGGCTAC	TCCATCAAGG	1560
TGTTGCACTT	CGAGCGCTCG	GGCCTGCAGC	ACGCGCCCGA	GCCCGACGCC	GCCGACGGCC	1620
CCTACGACCC	CAACAGCGTC	CGCATCAGCT	TCGCCAAGGG	CTGGGGGGCCC	TGCTACTCCC	1680
GGCAGTTCAT	CACCTCCTGC	CCCTGCTGGC	TGGAGATCCT	CCTCAACAAC	CCCAGATAGT	1740
GGCGGCCCCG	GCGGGAGGGG	CGGGTGGGAG	GCCGCGGCCA	CCGCCACCTG	CCGGCCTCGA	1800
GAGGGGCCGA	TGCCCAGAGA	CACAGCCCCC	ACGGACAAAA	CCCCCAGAT	ATCATCTACC	1860
TAGATTTAAT	ATAAAGTTTT	ATATATTATA	TGGAAATATA	TATTATACTT	GTAATTATGG	1920
AGTCATTTT	ACAATGTAAT	TATTTATGTA	TGGTGCAATG	TGTGTATATG	GACAAAACAA	1980
GAAAGACGCA	CTTTGGCTTA	TAATTCCTTC	AATACAGATA	TATTTTCTTT	CTCTTCCTCC	2040
TTCTCTTCC	TTACTTTTTA	TATATATATA	TAAAGAAAAAT	GATACAGCAG	AGCTAGGTGG	2100
AAAAGCCTGG	GTTTGGTGTA	TGGTTTTTGA	GATATTAATG	CCCAGACAAA	AAGCTAATAC	2160
CAGTCACCTG	ATAATAAAGT	ATTTCGATTA	TAGTTTTTTT	TAAACTGTCT	TCTTTTTTACA	2220
AAGAGGGGCA	GGTAGGGCTT	CAGCGGATTT	CTGACCCATC	ATGTACCTTG	AAACTTGACC	2280
TCAGTTTTCA	AGTTTTACTT	TTATTGGATA	AAGACAGAAC	AAATTGAAAA	GGGAGGAAAG	2340
TCACATTTAC	TCTTAAGTAA	ACCAGAGAAA	GTTCTGTTGT	TCCTTCCTGC	CCATGGCTAT	2400
GGGGTGTCCA	GTGGATAGGG	ATGGCGGTGG	GGAAAAGGAG	AATACACTGG	CCATTTATCC	2460
TGGACAAGCT	CTTCCAGTCT	GATGGAGGAG	GTTTCATGCC	TAGCCTAGAA	AGGCCCAGGT	2520
CCATGACCCC	CATCTTTGAG	TTATGAGCAA	GCTAAAAGAA	GACACTATTT	CTCACCATTT	2580
TGTGGAAATG	GCCTGGGGAA	CAAAGACTGA	AATGGGCCTT	GAGCCCACCT	GCTACCTTGC	2640
AGAGAACCAT	CTCGAGCCCC	GTAGATCTTT	TTAGGACCTC	CACAGGSTAT	TTCCCACCCC	2700
CCAGCCAAAA	ATAGCTCAGA	ATCTGCCCCA	CCAGGGCTTG	TATTAATGAT	TTATGTAAAG	2760
CGAGATGGTT	TATTTCTACT	TTGTAAAAGG	GAAAAGTTGA	GGTTCCTGGA	GGATAAATGA	2820
TTTGCTCATG	AGACAAAATC	AAGGTTAGAA	GTTACATGGA	ATTGTAGGAC	CAGAGCCATA	2880
TCATTAGATC	AGCTTTCTGA	AGAATATTCT	CCAMAAAAGA	AAGTCTCCTT	GGCCAGATAA	2940
CTAAGAGGAA	TGTTTCATTG	TATATCTTTT	TTCTTGAGAA	TTTATATTAA	CATATTAAGT	3000
GCTCTGAGAA	ATCCTGTGTA	TTATCTCTTG	CTGCATAATA	ATTATCCCCA	AACTTAAAAA	3060
AAAAAAAAAA	AAAAAACTC	GAG				3083

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Ser	Arg	Met	Gly	Lys	Pro	Ile	Glu	Thr	Gln	Lys	Ser	Pro	Pro	Pro
1				5				10						15	
Pro	Tyr	Ser	Arg	Leu	Ser	Pro	Arg	Asp	Glu	Tyr	Lys	Pro	Leu	Asp	Leu
			20					25					30		
Ser	Asp	Ser	Thr	Leu	Ser	Tyr	Thr	Glu	Thr	Glu	Ala	Thr	Asn	Ser	Leu
			35				40					45			
Ile	Thr	Ala	Pro	Gly	Glu	Phe	Ser	Asp	Ala	Ser	Met	Ser	Pro	Asp	Ala
			50			55					60				
Thr	Lys	Pro	Ser	His	Trp	Cys	Ser	Val	Ala	Tyr	Trp	Glu	His	Arg	Thr
			65		70					75				80	
Arg	Val	Gly	Arg	Leu	Tyr	Ala	Val	Tyr	Asp	Gln	Ala	Val	Ser	Ile	Phe
			85					90						95	
Tyr	Asp	Leu	Pro	Gln	Gly	Ser	Gly	Phe	Cys	Leu	Gly	Gln	Leu	Asn	Leu
			100				105						110		
Glu	Gln	Arg	Ser	Glu	Ser	Val	Arg	Thr	Arg	Ser	Lys	Ile	Gly	Phe	
			115				120				125				
Gly	Ile	Leu	Leu	Ser	Lys	Glu	Pro	Asp	Gly	Val	Trp	Ala	Tyr	Asn	Arg
			130			135					140				
Gly	Glu	His	Pro	Ile	Phe	Val	Asn	Ser	Pro	Thr	Leu	Asp	Ala	Pro	Gly
			145		150					155				160	
Gly	Arg	Ala	Leu	Val	Val	Arg	Lys	Val	Pro	Pro	Gly	Tyr	Ser	Ile	Lys

Val	Phe	Asp	Phe	Glu	Arg	Ser	Gly	Leu	Gln	His	Ala	Pro	Glu	Pro	Asp
			180					185					190		
Ala	Ala	Asp	Gly	Pro	Tyr	Asp	Pro	Asn	Ser	Val	Arg	Ile	Ser	Phe	Ala
		195					200					205			
Lys	Gly	Trp	Gly	Pro	Cys	Tyr	Ser	Arg	Gln	Phe	Ile	Thr	Ser	Cys	Pro
	210					215					220				
Cys	Trp	Leu	Glu	Ile	Leu	Leu	Asn	Asn	Pro	Arg					
225					230					235					

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACGAGGACGA	CAGGCTGTGC	GCGGTCTGCA	CGGCGCTCCG	CGGCGGAGCT	TCATGTGGGG	60
CTGCGACCCG	CGCAGCCGGC	GCCTCGCTGA	GGGAACGGAC	CCCCGGTAAC	CGGAGACCGC	120
CTTCCCCCCC	ACCCCTGGCG	CCAAAGGATA	TCGTATGTTT	AGGTCCAAAC	GCTCGGGGCT	180
GGTGCGGCGA	CTTTGGCGAA	GTCGTGTGGT	CCCCGACCGG	GAGGAAGGCG	GCAGCGGCGG	240
CGGCGGTGGC	GGCGACGAGG	ATGGGAGCTT	GGGCAGCCGA	GCTGAGCCGG	CCCCGCGGGC	300
AAGAGAGGGC	GGAGGCTGCG	GCCGCTCCGA	AGTCCGCCCC	GTAGCCCCGC	GGCGGCCCCG	360
GGACGCACTG	GGACAGCGAG	GCGCCCAGGG	CGCGGGGAGG	CGCCGGCGCG	CAGGGGGCCC	420
CCCCGAGGCC	ATGTCGGAGC	CAGGGGCGCG	CGCTGGGAGC	TCCCTGCTGG	ACGTGGCGGA	480
GCCGGGAGGC	CCGGGCTGGC	TGCCCCAGAG	TGACTGCGAG	ACGGTGACCT	GCTGTCTCTT	540
TTCGGAGCGG	GACGCCGCCG	GCGCGCCCCG	GGACGCCAGC	GACCCCTGG	CCGGGGCGGC	600
CCTGGAGCCG	GCGGGCGGCG	GGCGGAGTCG	CGAAGCGCGC	TCGCGGCTGC	TGCTGCTGGA	660
GCAGGAATCT	AAAACCGTCA	CGTACTCGCT	GCTGAAGCGG	CTCAAGGAGC	GCTCGCTGGA	720
CACGCTGCTG	GAGGCGGTGG	AGTCCCAGCG	CGGCGTGCCG	GGCGGCTGCG	TGCTGGTGCC	780
GCGCGCCGAC	CTCCGCTTGG	GCGGCCAGCC	CGCGCCGCCC	CAGCTGCTGC	TCGGCCGCCT	840
CTTTGCTGCT	CCCGACCTGC	AGCACGCCCT	GGAGCTGAAG	CCCCTGTGCG	GCTGCCACAG	900
CTTCGCCGCC	GCCGCCGACG	GCCCTACCGT	GTGCTGCAAC	CCCTACCACT	TCAGCCGGCT	960
CTGCGGGCCC	GAATCTCCGC	CACCTCCCTA	CTCTCGGCTG	TCTCCTCGCG	ACGAGTACAA	1020
GCCACTGGAT	CTGTCCGATT	CCACATTGTC	TTACACTGAA	ACGGAGGCTA	CCAATCCCTT	1080
CATCACTGCT	CCGGGTGAAT	TCTCAGACGC	CAGCATGTCT	CCGACGCCCA	CCAAGCCGAG	1140
CCACTGGTGC	AGCGTGGCGT	ACTGGGAGCA	CCGGACGCGC	GTGGGCCGCG	TCTATGCGGT	1200
GTACGACCAG	GCCGTCAGCA	TCTTCTACGA	CCTACCTCAG	GGCAGCGGCT	TCTGCCTGGG	1260
CCAGCTCAAC	CTGGAGCAGC	GCAGCGAGTC	GGTGCGGCGA	ACGCGCAGCA	AGATCGGCTT	1320
CGGCATCCTG	CTCAGCAAGG	AGCCCCAGCG	CGTGTGGGCC	TACAACCGCG	GCGAGCACCC	1380
CATCTTCGTC	AATCCCCGGA	CGCTGGACGC	GCCCCGGCGG	CGCGCCCTGG	TCGTGCGCAA	1440
GGTGCCCCCC	GGCTACTCCA	TCAAGGTGTT	CGACTTCGAG	CGCTCGGGCC	TGCAGCACGC	1500
GCCCCGAGCC	GACGCCGCCG	ACGGCCCCTA	CGACCCCAAC	AGCGTCCGCA	TCAGCTTCGC	1560
CAAGGGCTGG	GGGCCCTGCT	ACTCCCGGCA	GTTTCATCACC	TCCTGCCCCCT	GCTGGCTGGA	1620
GATCCTCCTC	AACAACCCCA	GATAGTGGCG	GCCCCGGCGG	GAGGGGCGGG	TGGGAGGCCG	1680
CGGCCACCGC	CACCTGCCGG	CCTCGAGAGG	GGCCGATGCC	CAGAGACACA	GCCCCACCGG	1740
ACAAAACCCC	CCAGATATCA	TCTACCTAGA	TTTAATATAA	AGTTTTATAT	ATTATATGGA	1800
AAAAAAAAAA	AAAAAAA					1817

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Phe	Arg	Ser	Lys	Arg	Ser	Gly	Leu	Val	Arg	Arg	Leu	Trp	Arg	Ser
1				5					10					15	

Arg	Val	Val	Pro	Asp	Arg	Glu	Glu	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Asp	Glu	Asp	Gly	Ser	Leu	Gly	Ser	Arg	Ala	Glu	Pro	Ala	Pro	Arg
		35					40					45			
Ala	Arg	Glu	Gly	Gly	Gly	Cys	Gly	Arg	Ser	Glu	Val	Arg	Pro	Val	Ala
		50				55					60				
Pro	Arg	Arg	Pro	Arg	Asp	Ala	Val	Gly	Gln	Arg	Gly	Ala	Gln	Gly	Ala
					70					75					80
Gly	Arg	Arg	Arg	Arg	Ala	Gly	Gly	Pro	Pro	Arg	Pro	Met	Ser	Glu	Pro
				85					90					95	
Gly	Ala	Gly	Ala	Gly	Ser	Ser	Leu	Leu	Asp	Val	Ala	Glu	Pro	Gly	Gly
			100					105					110		
Pro	Gly	Trp	Leu	Pro	Glu	Ser	Asp	Cys	Glu	Thr	Val	Thr	Cys	Cys	Leu
		115					120					125			
Phe	Ser	Glu	Arg	Asp	Ala	Ala	Gly	Ala	Pro	Arg	Asp	Ala	Ser	Asp	Pro
		130				135					140				
Leu	Ala	Gly	Ala	Ala	Leu	Glu	Pro	Ala	Gly	Gly	Arg	Ser	Arg	Glu	
					150					155				160	
Ala	Arg	Ser	Arg	Leu	Leu	Leu	Leu	Glu	Gln	Glu	Leu	Lys	Thr	Val	Thr
				165					170					175	
Tyr	Ser	Leu	Leu	Lys	Arg	Leu	Lys	Glu	Arg	Ser	Leu	Asp	Thr	Leu	Leu
			180					185					190		
Glu	Ala	Val	Glu	Ser	Arg	Gly	Gly	Val	Pro	Gly	Gly	Cys	Val	Leu	Val
		195					200					205			
Pro	Arg	Ala	Asp	Leu	Arg	Leu	Gly	Gly	Gln	Pro	Ala	Pro	Pro	Gln	Leu
		210				215					220				
Leu	Leu	Gly	Arg	Leu	Phe	Arg	Trp	Pro	Asp	Leu	Gln	His	Ala	Val	Glu
					230				235						240
Leu	Lys	Pro	Leu	Cys	Gly	Cys	His	Ser	Phe	Ala	Ala	Ala	Ala	Asp	Gly
				245					250					255	
Pro	Thr	Val	Cys	Cys	Asn	Pro	Tyr	His	Phe	Ser	Arg	Leu	Cys	Gly	Pro
			260					265					270		
Glu	Ser	Pro	Pro	Pro	Pro	Tyr	Ser	Arg	Leu	Ser	Pro	Arg	Asp	Glu	Tyr
		275				280						285			
Lys	Pro	Leu	Asp	Leu	Ser	Asp	Ser	Thr	Leu	Ser	Tyr	Thr	Glu	Thr	Glu
	290					295					300				
Ala	Thr	Asn	Ser	Leu	Ile	Thr	Ala	Pro	Gly	Glu	Phe	Ser	Asp	Ala	Ser
					310					315					320
Met	Ser	Pro	Asp	Ala	Thr	Lys	Pro	Ser	His	Trp	Cys	Ser	Val	Ala	Tyr
				325					330					335	
Trp	Glu	His	Arg	Thr	Arg	Val	Gly	Arg	Leu	Tyr	Ala	Val	Tyr	Asp	Gln
			340					345					350		
Ala	Val	Ser	Ile	Phe	Tyr	Asp	Leu	Pro	Gln	Gly	Ser	Gly	Phe	Cys	Leu
		355				360						365			
Gly	Gln	Leu	Asn	Leu	Glu	Gln	Arg	Ser	Glu	Ser	Val	Arg	Arg	Thr	Arg
	370					375					380				
Ser	Lys	Ile	Gly	Phe	Gly	Ile	Leu	Leu	Ser	Lys	Glu	Pro	Asp	Gly	Val
					390					395					400
Trp	Ala	Tyr	Asn	Arg	Gly	Glu	His	Pro	Ile	Phe	Val	Asn	Ser	Pro	Thr
			405					410						415	
Leu	Asp	Ala	Pro	Gly	Gly	Arg	Ala	Leu	Val	Val	Arg	Lys	Val	Pro	Pro
			420					425					430		
Gly	Tyr	Ser	Ile	Lys	Val	Phe	Asp	Phe	Glu	Arg	Ser	Gly	Leu	Gln	His
		435				440						445			
Ala	Pro	Glu	Pro	Asp	Ala	Ala	Asp	Gly	Pro	Tyr	Asp	Pro	Asn	Ser	Val
		450				455					460				
Arg	Ile	Ser	Phe	Ala	Lys	Gly	Trp	Gly	Pro	Cys	Tyr	Ser	Arg	Gln	Phe
					470					475					480
Ile	Thr	Ser	Cys	Pro	Cys	Trp	Leu	Glu	Ile	Leu	Leu	Asn	Asn	Pro	Arg
				485					490					495	

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 288...1565

(D) OTHER INFORMATION: Coding Sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCACGAGCGG	AGAGCCGCGC	AGGGCGCGGG	CCGCGCGGGG	TGGGGCAGCC	GGAGCGCAGG	60
CCCCCGATCC	CCGCGCGGGC	CCCCCGGGCC	CCCGCGCGCG	CCCCGGCCTC	CGGGAGACTG	120
GCGCATGCCA	CGGAGCGCCC	CTCGGGCCGC	CGCCGCTCCT	CCCCGGGCCC	CTGCTGCTGC	180
TGCTGTCCGC	TGCGCCTGCT	GCCCCAACTC	GGCGCCCGAC	TCACAAAGAA	ACATCATGTT	240
CGCTCCTTAG	CAGGCAAACG	ACTTTTCTCC	TGCCTCCTC	GCCCCGCATG	TTCAGGACCA	300
AACGATCTGC	GCTCGTCCGG	CGTCTCTGGA	GGAGCCGTGC	GCCCGGCGGC	GAGGACGAGG	360
AGGAGGGCGC	AGGGGGAGGT	GGAGGAGGAG	GCGAGCTGCG	GGGAGAAGGG	GCGACGGACA	420
GCCGAGCGCA	TGGGGCCGGT	GGCGGCGGCC	CGGGCAGGGC	TGGATGCTGC	CTGGGCAAGG	480
CGGTGCGAGG	TGCCAAAGGT	CACCACCATC	CCCACCCGCC	AGCCGCGGGC	CCCGGCGCGG	540
CCGGGGGCGC	CGAGGCGGAT	CTGAAGGCGC	TCACGCACTC	GGTGCTCAAG	AAACTGAAGG	600
AGCGGCAGCT	GGAGCTGCTG	CTCCAGGCCG	TGGAGTCCCG	CGGCGGGACG	CGCACCCGCT	660
GCCTCCTGCT	GCCCGGCCGC	CTGGACTGCA	GGCTGGGCCC	GGGGGCGCCC	GCCGGCGCGC	720
AGCCTGCGCA	GCCGCCCTCG	TCCTACTCGC	TCCCCCTCCT	GCTGTGCAAA	GTGTTTCAGG	780
GGCCGGATCT	CAGGCATTCC	TCGGAAGTCA	AGAGGCTGTG	TTGCTGTGAA	TCTTACGGGA	840
AGATCAACCC	CGAGCTGGTG	TGCTGCAACC	CCCATCACCT	TAGCCGACTC	TGCGAACTAG	900
AGTCTCCCCC	CCCTCCTTAC	TCCAGATACC	CGATGGATT	TCTCAAACCA	ACTGCAGACT	960
GTCCAGATGC	TGTGCCTTCC	TCCGCTGAAA	CAGGGGGAAC	GAATTATCTG	GCCCCTGGGG	1020
GGCTTTCAGA	TTCCCAACTT	CTTCTGGAGC	CTGGGGATCG	GTCACACTGG	TGCGTGGTGG	1080
CATACTGGGA	GGAGAAGACG	AGAGTGGGGA	GGCTCTACTG	TGTCCAGGAG	CCCTCTCTGG	1140
ATATCTTCTA	TGATCTACCT	CAGGGGAATG	GCTTTTGCCT	CGGACAGCTC	AATTCCGGACA	1200
ACAAGAGTCA	GCTGGTGCAG	AAGGTGCGGA	GCAAAATCGG	CTGCGGCATC	CAGCTGACGC	1260
GGGAGGTGGA	TGGTGTGTGG	GTGTACAACC	GCAGCAGTTA	CCCCATCTTC	ATCAAGTCCG	1320
CCACACTGGA	CAACCCGGAC	TCCAGGACGC	TGTTGGTACA	CAAGGTGTTT	CCCGGTTTCT	1380
CCATCAAGGC	TTTCGACTAC	GAGAAGGCGT	ACAGCCTGCA	GCGGCCCAAT	GACCACGAGT	1440
TTATGCAGCA	GCCGTGGACG	GGCTTTACCG	TGCAGATCAG	CTTTGTGAAG	GGCTGGGGTC	1500
AGTGCTACAC	CCGCCAGTTC	ATCAGCAGCT	GCCCGTGCTG	GCTAGAGGTC	ATCTTCAACA	1560
GCCGGTAGCC	GCGTGCGGAG	GGGACAGAGC	GTGAGCTGAG	CAGGCCACAC	TTCAAACCTAC	1620
TTTGCTGCTA	ATATTTTCTT	CCTGAGTGCT	TGCTTTTCAT	GCAAACCTCT	TGGTCGTTTT	1680
TTTTTTGTTT	GTTGGTTGGT	TTTCTTCTTC	TCGTCTCTCG	TTGTGTTCTG	TTTTGTTTCG	1740
CTCTTTGAGA	AATAGCTTAT	GAAAAGAATT	GTTGGGGGTT	TTTTTGGAAG	AAGGGGCAGG	1800
TATGATCGGC	AGGACACCCT	GATAGGAAGA	GGGGAAGCAG	AAATCCAAGC	ACCACCAAAC	1860
ACAGTGATATG	AAGGGGGGCG	GTCATCATTT	CACTTGTCAG	GAGTGTGTGT	GAGTGTGAGT	1920
GTGCGGCTGT	GTGTGCACGC	GTGTGCAGGA	GCGGCAGATG	GGGAGACAAC	GTGCTCTTTG	1980
TTTTGTGTCT	GTTATGGATG	TCCCAGCAG	AGAGGTTTGC	AGTCCCAAGC	GGTGCTCTCT	2040
CTGCCCCCTG	GACACGCTCA	GTGGGGCAGA	GGCAGTACCT	GGGCAAGCTG	GCGGCTGGGG	2100
TCCAGCAGC	TGCCAGGAGC	ACGGCTCTGT	CCCCAGCCTG	GGAAAGCCCC	TGCCCCCTCCT	2160
CTCCCTCATC	AAGGACACGG	GCCTGTCCAC	AGGCTTCTGA	GCAGCGAGCC	TGCTAGTGGC	2220
CGAACCAGAA	CCAATTATTT	TCATCCTTGT	CTTATTCCCT	TCCTGCCAGC	CCCTGCCATT	2280
GTAGCGTCTT	TCTTTTTTGG	CCATCTGCTC	CTGGATCTCC	CTGAGATGGG	CTTCCCAAGG	2340
GCTGCCGGGG	CAGCCCCCTC	ACAGTATTGC	TCACCCAGTG	CCCTCTCCCC	TCAGCCTCTC	2400
CCCTGCCTGC	CCTGGTGACA	TCAGGTTTTT	CCCGGACTTA	GAAAACCAGC	TCAGCACTGC	2460
CTGCTCCCAT	CCTGTGTGTT	AAGCTCTGCT	ATTAGGCCAG	CAAGCGGGGA	TGTCCCTGGG	2520
AGGGACATGC	TTAGCAGTCC	CCTTCCCTCC	AAGAAGGATT	TGGTCCGTCA	TAACCCAAGG	2580
TACCATCCTA	GGCTGACACC	TAACCTTTCT	TTCATTTCTT	CTACAACCTCA	TACACTCGTA	2640
TGATACTTCG	ACACTGTTCT	TAGCTCAATG	AGCATGTTTA	GACTTTAACA	TAAGCTATTT	2700
TTCTAACTAC	AAAGGTTTAA	ATGAACAAGA	GAAGCATTTCT	CATTGGAAAT	TTAGCATTGT	2760
AGTGCTTTGA	GAGAGAAAGG	ACTCCTGAAA	AAAAACCTGA	GATTTATTAA	AGAAAAAAT	2820
GTATTTATAG	TTATATATA	ATATATTATT	ACTTGTAAT	ATAAAGACGT	TTTATAAGCA	2880
TCATTATTTA	TGATTGTGC	AATGTGTATA	AACAAGAAAA	ATAAAGAAAA	GATGCACTTT	2940
GCTTTAATAT	AAATGCAAT	AACAAATGCC	AAATTAATAA	AGATAAACAC	AAGATTGGTG	3000
TTTTTTTCTA	TGGGTGTTAT	CACCTAGCTG	AATGTTTTTC	TAAAGGAGTT	TATGTTCCAT	3060
TAAACGATTT	TTAAATGTA	CACCTGAAAA	AAAAAAAAAA	AAA		3103

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Phe	Arg	Thr	Lys	Arg	Ser	Ala	Leu	Val	Arg	Arg	Leu	Trp	Arg	Ser
1				5					10					15	
Arg	Ala	Pro	Gly	Glu	Asp	Glu	Glu	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Gly
			20				25						30		
Gly	Gly	Gly	Glu	Leu	Arg	Gly	Glu	Gly	Ala	Thr	Asp	Ser	Arg	Ala	His
			35				40					45			
Gly	Ala	Gly	Gly	Gly	Gly	Pro	Gly	Arg	Ala	Gly	Cys	Cys	Leu	Gly	Lys
			50			55					60				
Ala	Val	Arg	Gly	Ala	Lys	Gly	His	His	His	Pro	His	Pro	Pro	Ala	Ala
65					70					75					80
Gly	Ala	Gly	Ala	Ala	Gly	Gly	Ala	Glu	Ala	Asp	Leu	Lys	Ala	Leu	Thr
				85					90					95	
His	Ser	Val	Leu	Lys	Lys	Leu	Lys	Glu	Arg	Gln	Leu	Glu	Leu	Leu	Leu
			100					105					110		
Gln	Ala	Val	Glu	Ser	Arg	Gly	Gly	Thr	Arg	Thr	Ala	Cys	Leu	Leu	Leu
			115				120					125			
Pro	Gly	Arg	Leu	Asp	Cys	Arg	Leu	Gly	Pro	Gly	Ala	Pro	Ala	Gly	Ala
			130			135					140				
Gln	Pro	Ala	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Leu	Pro	Leu	Leu	Leu	Cys
145					150					155					160
Lys	Val	Phe	Arg	Trp	Pro	Asp	Leu	Arg	His	Ser	Ser	Glu	Val	Lys	Arg
				165					170					175	
Leu	Cys	Cys	Cys	Glu	Ser	Tyr	Gly	Lys	Ile	Asn	Pro	Glu	Leu	Val	Cys
			180					185					190		
Cys	Asn	Pro	His	His	Leu	Ser	Arg	Leu	Cys	Glu	Leu	Glu	Ser	Pro	Pro
		195					200					205			
Pro	Pro	Tyr	Ser	Arg	Tyr	Pro	Met	Asp	Phe	Leu	Lys	Pro	Thr	Ala	Asp
		210				215					220				
Cys	Pro	Asp	Ala	Val	Pro	Ser	Ser	Ala	Glu	Thr	Gly	Gly	Thr	Asn	Tyr
225					230					235					240
Leu	Ala	Pro	Gly	Gly	Leu	Ser	Asp	Ser	Gln	Leu	Leu	Leu	Glu	Pro	Gly
				245						250				255	
Asp	Arg	Ser	His	Trp	Cys	Val	Val	Ala	Tyr	Trp	Glu	Glu	Lys	Thr	Arg
			260					265					270		
Val	Gly	Arg	Leu	Tyr	Cys	Val	Gln	Glu	Pro	Ser	Leu	Asp	Ile	Phe	Tyr
			275				280					285			
Asp	Leu	Pro	Gln	Gly	Asn	Gly	Phe	Cys	Leu	Gly	Gln	Leu	Asn	Ser	Asp
			290			295					300				
Asn	Lys	Ser	Gln	Leu	Val	Gln	Lys	Val	Arg	Ser	Lys	Ile	Gly	Cys	Gly
305					310					315					320
Ile	Gln	Leu	Thr	Arg	Glu	Val	Asp	Gly	Val	Trp	Val	Tyr	Asn	Arg	Ser
				325						330				335	
Ser	Tyr	Pro	Ile	Phe	Ile	Lys	Ser	Ala	Thr	Leu	Asp	Asn	Pro	Asp	Ser
			340					345					350		
Arg	Thr	Leu	Val	His	Lys	Val	Phe	Pro	Gly	Phe	Ser	Ile	Lys	Ala	
		355				360						365			
Phe	Asp	Tyr	Glu	Lys	Ala	Tyr	Ser	Leu	Gln	Arg	Pro	Asn	Asp	His	Glu
					375						380				
Phe	Met	Gln	Gln	Pro	Trp	Thr	Gly	Phe	Thr	Val	Gln	Ile	Ser	Phe	Val
385					390					395					400
Lys	Gly	Trp	Gly	Gln	Cys	Tyr	Thr	Arg	Gln	Phe	Ile	Ser	Ser	Cys	Pro
				405					410					415	
Cys	Trp	Leu	Glu	Val	Ile	Phe	Asn	Ser	Arg						
			420					425							